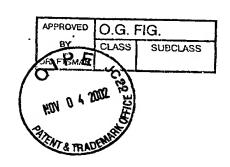


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FIGURE 2A

	Exon1	Exon 2 ATG	Exon 3	Exon 4 Published as exon 2	Exon 5 Published as exon 3 ATG	Exon 6 Published as exon 3	RP11-1M10 Exon 1: 3463-3679 Exon2: 147715-147555 Exon3: 160429-160801
FIGURE 2B							
Ti	HP-1						
Α		_	•	_	_		
В	lepG2	-		_			
С D				#####		-	
	FIGUE	RE 2C					
	1			22		·	61
A, B MACWPQLRVLLWKNLTFRRRQTCQLLLEVAWPLFIFLILISVRLSYPPYEQHECHFPNKAM C, D MCQLLLEVAWPLFIFLILISVRLSYPPYEQHECHFPNKAM							
	tBlastn result: Alignment between hABC1 and hABCR. Identical = 32/56 (57%), conservative = 12/56 (21%)						
	hABC1 6QLRVLLWKNLTFRRRQTCQLLLEVAWPLFIFLILISVRLSYPPYEQHECHFPNKAM 61						
	hABCR 6QIQLLLWKNWTLRKRQKIRFVVELVWPLSLFLVLIWLRNANPLYSHHECHFPNKAM 61						
	tBlastn result: Alignent between hABC1 and hABC3. Identical = 20/44 (45%), conservative = 7/44 (16%) hABC1						



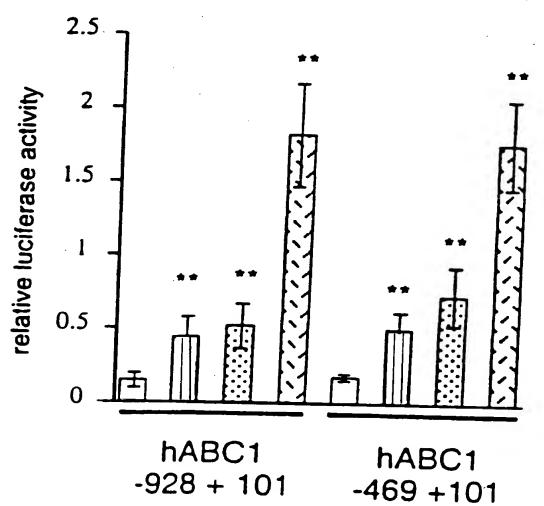
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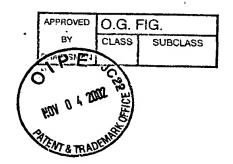
FIGURE 5B



9-cis r.a.

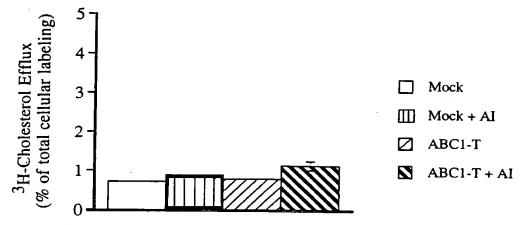
9-cis r.a. + 22(R)-Hch





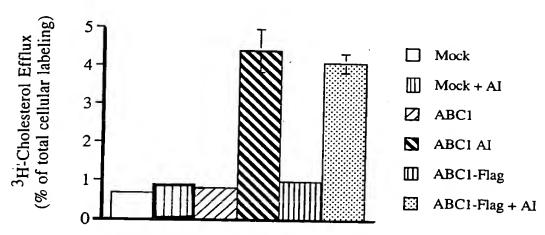
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FIGURE 8A



ABC1-T: 61 MPSAGT--- (Genebank Accession: X75926; the methionine 61 here was originally designated as the start methionine. This version of cDNA is inactive in stimulating cholesterol efflux.)

FIGURE 8B



ABC1:

- MACWPQLRLLLWKNLTFRRRQTCQLLLEVA
- 31 WPLFIFLILISVRLSWPPYEQHECHFPNKA
- 61 MPSAGT---

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